



**Figure S5. Tissue specificity in expression of mouse Rabs.** We analysed microarray data from the Mouse Exon Atlas (GEO accession: GSE15998) generated on an Affymetrix Mouse Exon 1.0 ST Array (GEO accession: GPL6193) downloaded from [1]. We mapped probes to genes using the R package provided in [2]. The data analysis has been performed in R using Bioconductor's 'affy' library. After applying RMA [3], we combined biological replicates by averaging their expression value. To transform continuous expression

into a discrete present/absent pattern we chose a threshold (5.0) that maximises the agreement with the PCR data from **Figure 8** while achieving a balanced number of false positives (28) and false negatives (25).

## References

1. Wu C, Orozco C, Boyer J, Leglise M, Goodale J et al. (2009) BioGPS: an extensible and customizable portal for querying and organizing gene annotation resources. *Genome Biol* 10: R130.
2. Risueno A, Fontanillo C, Dinger ME, De Las Rivas J (2010) GATEExplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. *BMC Bioinformatics* 11: 221.
3. Irizarry RA, Hobbs B, Collin F, Beazer-Barclay YD, Antonellis KJ et al. (2003) Exploration, normalization, and summaries of high density oligonucleotide array probe level data. *Biostatistics* 4: 249-264.